

Structure of the human POSHL1 protein

Fig. 1A

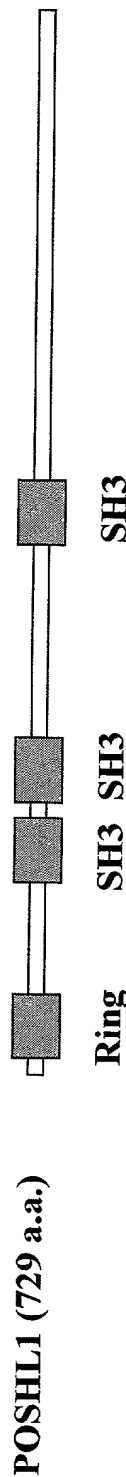


Fig. 1B

Ring Domain

	10	20	30	40
consensus*.....*.....*.....			
POSHL1	1 CPICLEEY----	12 LKDPVVLP-CGHT-FCRSCIRKWLESSN-SNTCPIC	41	
1G25_A	6 CPVCFEKL----	12 DVTAKVLP-CQHT-FCKPCLQRVFKAHK-ELRCPEC	52	
gi 2145348	18 CPRCKTTKyrnpSLKLMVNV-CGHT-LCESCVDLLFVRG--AGNCPEC	49		
gi 2342720	91 CPVCLDL-----	18 FRVPITLM-CGHT-CCKHCLngiv--ksdNARCPVC	56	
gi 2738440	111 CVVCYEN-----	111 EICKIQP-CNHfVCKSCFNR-----LNTCPMC	145	
gi 3043558	71 CSICLER-----	71 YKNPKVLP-CLHT-FCERCLQNYIPAHsltLSCPVC	111	
gi 3152606	28 CNICFEL-----	28 AQDPIVTL-CGHL-FCWPCLYRWLHHHshSQECPCV	68	
gi 3002588	12 CPVCLERL-----	12 DASAKVLP-CQHT-FCKRCLLGIVGSRn-eLRCPEC	52	
gi 6226931	43 CPICLDR-----	43 YKQPKLLP-CQHT-FCYPCLCSCADTLhrnLKCPEC	83	

FIG. 1C

SH3 Domain 1

	10	20	30	40	50	60
consensus*.....*.....*.....*.....					
POSHL1	1 EGPQVRALYDYTAQDPDELDFKKGDIITVLEKS-----DDGWKGRLG-T	44				
1PHT	126 GVPRAKALCNYRGQNPGLRFNKGDIILRRQL-----DENWYQGEI--N	168				
gi 3882275	4 EGYQYRALYDYKKEREEDIDLHLGDIITVKNKGSvalgfsdggearpeEIGWLNQYNETT	63				
gi 4176446	864 EKLPKAVYDFKAQTSKELSFKKGDTVYLKII-----DQNWYEGEHH--	906				
gi 2114412	509 HRRRAKALLDFERHDDDELGFRKNDIITVSQK-----DEHCWVGELN--	551				
gi 2190355	994 KLPQVKALYPYTAANDEELSFKKVGDITILEK-----DEGWKKGELN--	1035				
gi 4894215	244 ENLYATALYPYQASQWHLPFKKDDKIVLLDIKS-----EEGWLKGELN--	287				
gi 3158515	113 EYGEAVAQYTFKGDLEVELSFRKGEHICLRKV-----NENWYEGRITgT	157				
gi 3002588	383 QKPQCRALFDFDAQSEGEGLDFKEGTILIELVSQI-----DENWYEGRVN--	425				
	135 QLPCAKALYNYEGKEPGLKFSKGDITILRRQV-----DENWYHGEVS--	177				
70						
consensus*.....*					
POSHL1	45 GKEGLFPPSNYVEEID	59				
1PHT	169 GISGNFPASSVEVIK	183				
gi 3882275	64 GERGDFPGTYVEYIG	78				
gi 4176446	907 GRVGIFPISYVEKLT	921				
gi 2114412	552 GLRGWFPAPKFFVEVLD	566				
gi 2190355	1036 QQEGWIPNNYVKEI-	1049				
gi 4894215	288 GKIGYFPASYVEIIA	302				
gi 3158515	158 GRQGIFFASYVQVSR	172				
gi 3002588	426 GKTGLFPVTYVQVLV	440				
	178 GVHGFPTNFVQIIK	192				

FIG. 1D

SH3 Domain 2

		10	20	30	40	50	60
consensus	*.....*.....*.....*.....					
1	EGPQVRALYDYT	-----A-----QDPDELSFKGDIITVLEKS	-----DD	35			
188	PPPLCRALYNFDLrgkds	-----ENQDCLTFLKDDIITVISRV	-----DE	228			
1PHT	4	EGYQYRALYDYK	-----K-----EREEDIDLHLGDILTVNKGSLvalgsdggearpeEI	53			
gi 3880771	408	VSPYARAVYDFQ	-----G-----EFENELSFSADEIISLRRRI	-----DA	442		
gi 729368	153	EEMLVQALYDFV	-----P-----QESGELDFRRGDVITVTDRS	-----DE	187		
gi 1346669	458	KGSQVEALFSYE	-----A-----TQPEDLEFQEGDIILVLSKV	-----NE	492		
gi 2961227	995	GPEQARALYDFA	-----A-----ENPDELTFNEGAVVTVINKS	-----NP	1029		
gi 2960022	3	QPLVVQAEYSFM	-----G-----SNNDELCFQKGDVITVTQRE	-----DG	37		
gi 3002588	197	PPPQCKALYDFE	-----VkdkeADKDCLPFAKDDVLTVIRRV	-----DE	235		
gi 3599478	1160	TVGRCRALYDYG	-----A-----QEADELTLREGDVIDVIQK	-----SG	1193		

		70	80
	*.....*.....*	
consensus	36	GWKGRIG-TGKEGLFPSNYVEEID	59
POSHL1	229	NWAEKGLG-D-KVGIFPILFVEPnl	251
1PHT	54	GWLNGYNETTGERGDFPGTYVEYIG	78
gi 3880771	443	EWLEGSIG-SARVGIFPTSFVQIIV	466
gi 729368	188	NWNNGEIG--NRKGIFPATYVTPYH	210
gi 1346669	493	EWLEGECK--GKVGIFPKVFVEDCA	515
gi 2961227	1030	DWWEDELN--GQRGVFPASYVELIP	1052
gi 2960022	38	GWWEGLTN--DKTGWFPSPNYVNECK	60
gi 3002588	236	NWAEGLMA--DKIGIFPISYVEFNS	258
gi 3599478	1194	EWWEGLTN--GKTGVFPANYVEDI	1215

FIG. 1E

SH3 Domain 3

		10	20	30	40	50	60	
							
consensus	1	EGPQVRALYDYTAQDPDEL	SFKKGD	ITVLEKS	-----	DDGWKGR	LG-	43
POSHL1	381	SANMFVALHSYSAHGPDEL	LQKGEGRV	LKGC	-----	QDGLRGV	SLV-	424
1PHT	4	EGYQYRALYDYKKEREED	IDLHLGD	ILTVNKGSL	valgfsdg	gearpe	EIGWLNGY	NET 62
gi 4322306	664	DLCSYQALYSYVPQNDDEL	LRDGD	IVDVMEKC	-----	DDGWFVGT	-SRr	707
gi 127962	107	LNMPAYVKFNMAERED	ELSLIKG	TKVIVMEKC	-----	SDGWWRGS	-YN-	149
gi 7619882	126	GAPHAVALHDFPAEQADD	LSLTSGE	IVYLLEKI	-----	DAEWYRGK	-CR-	168
gi 3170194	156	VLYQVVAQHRYSAQGPED	LGRQGD	TVDLCEV	-----	DQAWLEGH	-CD-	198
gi 3002588	453	RPSVYVAIYPYTPRKEDE	LELRKGE	MFLVFERC	-----	QDGWYKGT	-SMh	496
gi 13324869	380	YLEKVRVLYDYDAAKEDE	LTRENAI	VYVLKKN	-----	DDDWEYEGV	-LD-	422
gi 488296	42	ANPVWTALFDYEPGQDEL	ALRKGR	VEVLSRDaai	-----	sgDEGWAGQ	-VG-	89

70

							
							
consensus	44	TGKEGLFPSNYVEEID	59					
POSHL1	425	TGRVGIFPNNYVPIf	440					
1PHT	63	TGERGDFPGTYVEYIG	78					
gi 4322306	708	TRQFGTFPGNYVKPLY	723					
gi 127962	150	-GQVGWFPSPNYVTEEG	164					
gi 7619882	169	-NQTGVFPANVVKVIV	183					
gi 3170194	199	-GRIGIFPKCFVVPAG	213					
gi 3002588	497	TSKIGVFPNGNYVAPVT	512					
gi 13324869	423	-GVTGLFPNGNYVVPV	436					
gi 488296	90	-GQVGIFPSNYVSRGG	104					

Structure of the POSHL1 gene (Chr. 5q32)

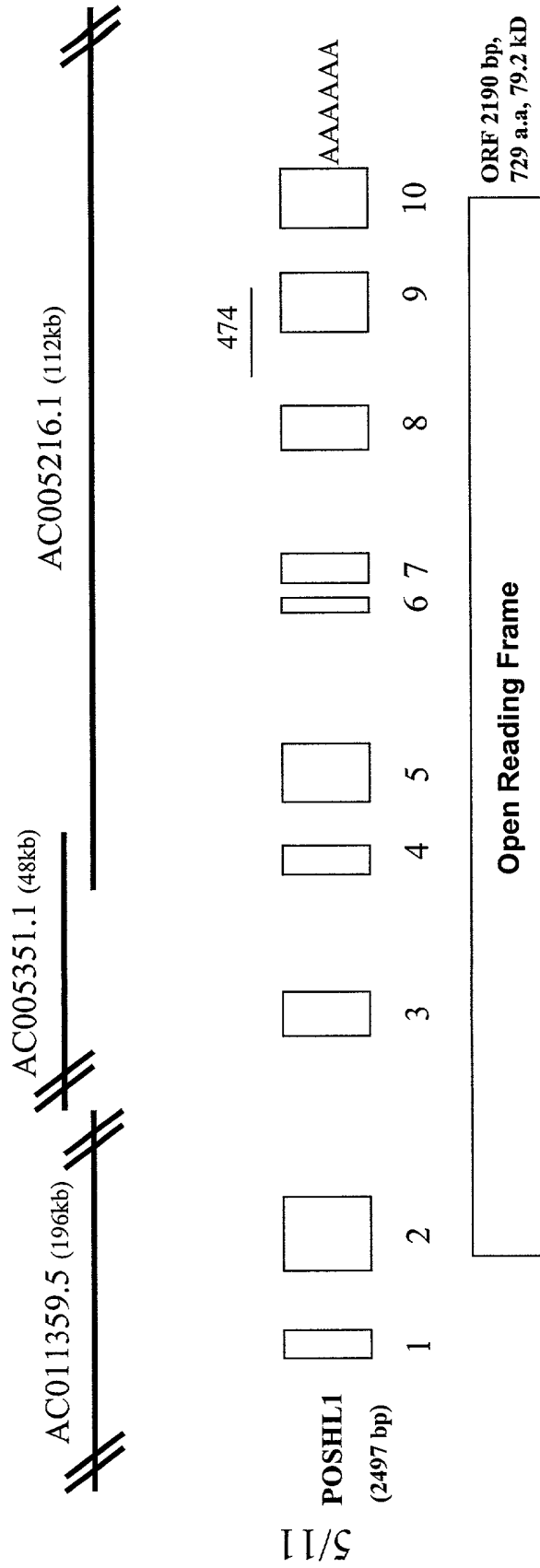


FIG. 2

POSHL1

nt: SEQ ID NO: 1

aa: SEQ ID NO: 3

AAAGTTTTTCAAAGCGGTTGGCAGCAGCGGCCTTGAGAGAAAGGAAGCCGGT		52
TGGAGGGGCGCAGCGCACCCCTGCTGCGCGGAGGAGGGGGCTGAGCTGAACTC		104
AGCAGAAGTTACATGCACAAGGCCAAAAATTCTGACGTTCTCAAGAGACCAGC		156
TCTGCCCCCGTGGCTCAACTGACCCTACCATGTGGACGCTGCTCCTCCAGGT		208
	M D D L T L L	7
GGGAACTGGAGTTTTGAAATAAA ATG GAT GAT TTG ACG TTA CTT		252
D L L E C P V C F E K L D		20
GAT CTT CTG GAG TGC CCT GTG TGC TTT GAG AAG CTC GAT		291
V T A K V L P C Q H T F C		33
GTC ACA GCC AAA GTC CTC CCT TGC CAG CAC ACC TTC TGC		330
K P C L Q R V F K A H K E		46
AAA CCA TGT CTA CAG AGG GTT TTC AAG GCC CAC AAA GAG		369
L R C P E C R T P V F S N		59
CTG CGG TGC CCC GAA TGC AGG ACG CCT GTG TTT TCC AAC		408
I E A L P A N L L L V R L		72
ATT GAG GCG CTG CCG GCC AAC CTG CTG CTC GTG CGC CTT		447
L D G V R S G Q S S G R G		85
CTG GAT GGA GTG CGC TCA GGG CAG AGC TCC GGG AGA GGG		486
G S F R R P G T M T L Q D		98
GGC TCC TTC CGC AGG CCT GGC ACG ATG ACC TTG CAG GAT		525

FIG. 3

G	R	K	S	R	T	N	P	R	R	L	Q	A	111
GGC	AGG	AAA	AGC	AGG	ACC	AAC	CCC	AGA	CGT	CTG	CAG	GCC	564
S	P	F	R	L	V	P	N	V	R	I	H	M	124
AGT	CCT	TTC	CGG	CTA	GTG	CCT	AAT	GTC	AGA	ATC	CAC	ATG	603
D	G	V	P	R	A	K	A	L	C	N	Y	R	137
GAT	GGG	GTG	CCT	CGA	GCA	AAG	GCC	TTA	TGC	AAC	TAC	AGA	642
G	Q	N	P	G	D	L	R	F	N	K	G	D	150
GGG	CAG	AAT	CCC	GGT	GAC	CTA	AGG	TTT	AAT	AAG	GGA	GAT	681
I	I	L	L	R	R	Q	L	D	E	N	W	Y	163
ATC	ATC	CTT	CTC	CGG	AGA	CAG	CTT	GAT	GAG	AAT	TGG	TAC	720
Q	G	E	I	N	G	I	S	G	N	F	P	A	176
CAG	GGG	GAA	ATC	AAT	GGC	ATC	AGC	GGG	AAC	TTC	CCA	GCC	759
S	S	V	E	V	I	K	Q	L	P	Q	P	P	189
AGC	TCC	GTG	GAA	GTC	ATC	AAG	CAG	CTG	CCC	CAG	CCG	CCC	798
P	L	C	R	A	L	Y	N	F	D	L	R	G	202
CCG	CTC	TGC	AGG	GCC	CTC	TAC	AAC	TTC	GAC	CTA	CGA	GGC	837
K	D	K	S	E	N	Q	D	C	L	T	F	L	215
AAG	GAC	AAG	AGT	GAG	AAC	CAG	GAT	TGC	CTG	ACC	TTC	CTC	876
K	D	D	I	I	T	V	I	S	R	V	D	E	228
AAG	GAC	GAT	ATC	ATC	ACT	GTG	ATC	AGC	CGA	GTG	GAT	GAG	915
N	W	A	E	G	K	L	G	D	K	V	G	I	241
AAC	TGG	GCA	GAA	GGC	AAG	TTA	GGA	GAT	AAA	GTA	GGC	ATC	954
F	P	I	L	F	V	E	P	N	L	T	A	R	254
TTC	CCT	ATC	TTG	TTT	GTA	GAG	CCA	AAC	CTC	ACC	GCA	AGA	993
H	L	L	E	K	N	K	G	R	Q	S	S	C	267
CAC	CTT	TTA	GAG	AAG	AAC	AAA	GGT	CGC	CAG	TCA	TCC	TGC	1032
T	K	N	L	S	L	V	S	S	S	S	R	G	280
ACA	AAA	AAC	CTG	TCC	CTG	GTG	TCC	TCG	TCC	TCC	AGA	GGC	1071

FIG. 3

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N	T	S	T	L	R	R	G	P	G	S	R	R	293
AAC	ACG	TCT	ACC	CTC	CGT	AGG	GGC	CCA	GGG	TCC	AGG	AGG	1110
K	V	P	G	Q	F	S	I	T	T	A	L	N	306
AAG	GTG	CCT	GGG	CAG	TTT	TCC	ATC	ACA	ACA	GCC	TTG	AAC	1149
T	L	N	R	M	V	H	S	P	S	G	R	H	319
ACT	CTC	AAC	CGG	ATG	GTC	CAT	TCT	CCT	TCA	GGG	CGC	CAT	1188
M	V	E	I	S	T	P	V	L	I	S	S	S	332
ATG	GTA	GAG	ATC	AGC	ACC	CCA	GTG	CTC	ATC	AGC	TCC	AGC	1227
N	P	S	V	I	T	Q	P	M	E	K	A	D	345
AAC	CCC	TCT	GTG	ATC	ACC	CAG	CCC	ATG	GAG	AAA	GCA	GAC	1266
V	P	S	S	C	V	G	Q	V	S	T	Y	H	358
GTT	CCT	TCC	AGC	TGT	GTG	GGA	CAG	GTC	AGC	ACT	TAT	CAC	1305
P	A	P	V	S	P	G	H	S	T	A	V	V	371
CCC	GCA	CCT	GTC	TCT	CCA	GGA	CAT	TCC	ACA	GCC	GTG	GTC	1344
S	L	P	G	S	Q	Q	H	L	S	A	N	M	384
AGT	CTG	CCT	GGC	TCC	CAG	CAA	CAC	CTC	TCA	GCG	AAC	ATG	1383
F	V	A	L	H	S	Y	S	A	H	G	P	D	397
TTT	GTA	GCC	CTG	CAC	TCC	TAC	TCA	GCC	CAT	GGA	CCC	GAT	1422
E	L	D	L	Q	K	G	E	G	V	R	V	L	410
GAG	CTG	GAC	CTG	CAA	AAG	GGA	GAA	GGC	GTC	AGG	GTC	CTG	1461
G	K	C	Q	D	G	W	L	R	G	V	S	L	423
GGG	AAG	TGC	CAG	GAC	GGC	TGG	CTC	AGG	GGC	GTC	TCC	TTG	1500
V	T	G	R	V	G	I	F	P	N	N	Y	V	436
GTC	ACC	GGG	CGA	GTC	GGC	ATC	TTC	CCA	AAC	AAT	TAC	GTC	1539
I	P	I	F	R	K	T	S	S	F	P	D	S	449
ATC	CCC	ATT	TTC	AGA	AAG	ACC	TCT	AGT	TTT	CCA	GAC	TCC	1578
R	S	P	G	L	Y	T	T	W	T	L	S	T	462
CGG	AGC	CCT	GGT	CTC	TAC	ACC	ACA	TGG	ACG	TTA	TCC	ACC	1617

FIG. 3

1001301-1102

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S	S	V	S	S	Q	G	S	I	S	E	G	D	475
TCC	TCT	GTG	TCC	TCC	CAA	GGC	AGC	ATT	TCA	GAA	GGT	GAT	1656
P	R	Q	S	R	P	F	K	S	V	F	V	P	488
CCA	CGG	CAA	AGC	CGT	CCC	TTC	AAA	TCC	GTC	TTT	GTG	CCC	1695
T	A	I	V	N	P	V	R	S	T	A	G	P	501
ACT	GCC	ATA	GTC	AAC	CCC	GTG	AGA	AGC	ACA	GCC	GGC	CCT	1734
G	T	L	G	Q	G	S	L	R	K	G	R	S	514
GGG	ACT	TTA	GGA	CAA	GGG	TCT	CTT	CGG	AAA	GGG	CGG	AGC	1773
S	M	R	K	N	G	S	L	Q	R	P	L	Q	527
AGC	ATG	AGA	AAG	AAT	GGA	TCC	CTG	CAG	AGA	CCC	CTC	CAG	1812
S	G	I	P	T	L	V	V	G	S	L	R	R	540
TCC	GGG	ATC	CCC	ACT	CTC	GTG	GTA	GGC	TCC	CTC	AGA	CGC	1851
S	P	T	M	V	L	R	P	Q	Q	F	Q	F	553
AGC	CCC	ACC	ATG	GTC	CTT	CGG	CCT	CAG	CAG	TTC	CAA	TTC	1890
Y	Q	P	Q	G	I	P	S	S	P	S	A	V	566
TAC	CAG	CCA	CAG	GGG	ATC	CCC	TCC	TCC	CCC	TCA	GCC	GTG	1929
V	V	E	M	G	S	K	P	A	L	T	G	E	579
GTG	GTG	GAG	ATG	GGG	TCC	AAG	CCT	GCC	CTC	ACG	GGG	GAG	1968
P	A	L	T	C	I	S	R	G	S	E	A	R	592
CCC	GCC	CTC	ACG	TGC	ATC	AGC	AGG	GGC	AGT	GAG	GCC	CGG	2007
T	H	S	A	A	S	S	L	I	M	E	D	K	605
ACC	CAC	TCC	GCG	GCC	AGC	TCC	CTC	ATT	ATG	GAA	GAC	AAA	2046
E	I	P	I	K	S	E	P	L	P	K	P	P	618
GAA	ATC	CCC	ATC	AAG	AGT	GAG	CCT	CTG	CCA	AAA	CCG	CCC	2085
A	S	A	P	P	S	I	L	V	K	P	E	N	631
GCA	TCT	GCC	CCA	CCA	TCC	ATC	CTG	GTG	AAA	CCA	GAA	AAC	2124
S	R	N	G	I	E	K	Q	V	K	T	V	R	644
TCA	AGA	AAT	GGC	ATC	GAA	AAG	CAA	GTC	AAA	ACC	GTG	AGA	2163

FIG. 3

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F	Q	N	Y	S	P	P	P	T	K	H	Y	T	657
TTT	CAG	AAT	TAC	AGC	CCT	CCT	CCC	ACC	AAA	CAT	TAC	ACC	2202
S	H	P	T	S	G	K	P	E	Q	P	A	T	670
TCC	CAT	CCC	ACC	TCC	GGA	AAG	CCT	GAA	CAG	CCA	GCC	ACC	2241
L	K	A	S	Q	P	E	A	A	S	L	G	P	683
CTC	AAG	GCG	TCC	CAG	CCT	GAA	GCA	GCG	TCC	TTG	GGC	CCA	2280
E	M	T	V	L	F	A	H	R	S	G	C	H	696
GAG	ATG	ACC	GTC	CTA	TTT	GCC	CAC	CGA	AGT	GGC	TGC	CAC	2319
S	G	Q	Q	T	D	L	R	R	K	S	A	L	709
TCC	GGA	CAG	CAG	ACA	GAC	CTC	CGG	AGA	AAG	TCA	GCT	CTT	2358
A	K	A	T	T	L	V	S	T	A	S	G	T	722
GCC	AAG	GCC	ACA	ACC	CTG	GTG	TCC	ACT	GCC	TCA	GGC	ACG	2397
Q	T	V	F	P	S	K	*						730
CAG	ACC	GTG	TTT	CCC	AGC	AAA	TGA	ACCTACGGGTGACTTTTCC					2440
TAGACCCCAAAGAGGTGAATTGCATTTAAATACAGTCTGCCTCCACTAAAAA													2492
AAAAA													2497

FIG. 3

RT-PCR Analysis of POSHL1 Expression

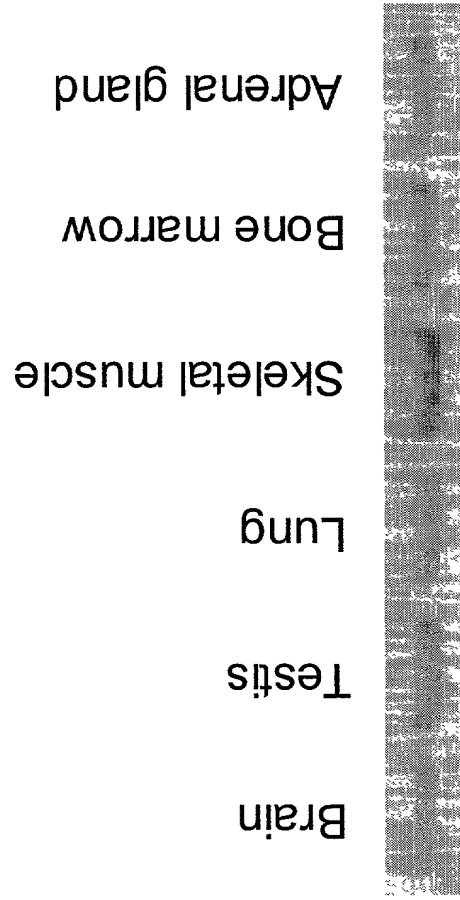


FIG. 4